

Serial Number:

09/724,524

ENTERED

CRF Processing Date:

8/28/2001

Edited by:

Verified by:

(STIC sta:

☐

Changed a file from non-ASCII to ASCII

☐

Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐

Edited a format error in the Current Application Data section, specifically:

☐Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____☐

Added the mandatory heading and subheadings for "Current Application Data".

☐

Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐

Changed the spelling of a mandatory field (the headings or subheadings), specifically:

☐

Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

☐

Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

☐

Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐

Inserted colons after headings/subheadings. Headings edited included:

☐

Deleted extra, invalid, headings used by an applicant, specifically:

☒Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file;
☐ page numbers throughout text; ☐ other invalid text, such as _____☐

Inserted mandatory headings, specifically: _____

☐

Corrected an obvious error in the response, specifically:

☐

Edited identifiers where upper case is used but lower case is required, or vice versa.

☐

Corrected an error in the Number of Sequences field, specifically:

☐

A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____☐

Other: _____

Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

RAW SEQUENCE LISTING

DATE: 08/28/2001

PATENT APPLICATION: US/09/724,524

TIME: 18:05:31

Input Set : A:\Pto.amc

Output Set: N:\CRF3\08282001\I724524.raw

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:
7 (i) APPLICANT: Presta, Leonard G.
8 Shelton, David L.
9 Urfer, Roman
11 (ii) TITLE OF INVENTION: Human trk Receptors and Neurotrophic Factor
12 Inhibitors
14 (iii) NUMBER OF SEQUENCES: 41
16 (iv) CORRESPONDENCE ADDRESS:
17 (A) ADDRESSEE: Knobbe, Martens, Olson & Bear
18 (B) STREET: 620 Newport Center Drive 16th Floor
19 (C) CITY: Newport Beach
20 (D) STATE: California
21 (E) COUNTRY: USA
22 (F) ZIP: 92660
24 (v) COMPUTER READABLE FORM:
25 (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
26 (B) COMPUTER: IBM PC compatible
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
28 (D) SOFTWARE: WinPatin (Genentech)
C--> 30 (vi) CURRENT APPLICATION DATA:
C--> 31 (A) APPLICATION NUMBER: US/09/724,524
C--> 32 (B) FILING DATE: 27-Nov-2000
43 (C) CLASSIFICATION:
C--> 49 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 09/156,923
37 (B) FILING DATE: 18-SEP-1998
41 (A) APPLICATION NUMBER: 08/359,705
42 (B) FILING DATE: 20-DEC-1994
46 (A) APPLICATION NUMBER: 08/286846
47 (B) FILING DATE: 10-AUG-1994
50 (A) APPLICATION NUMBER: 08/215139
51 (B) FILING DATE: 18-MAR-1994
C--> 53 (viii) ATTORNEY/AGENT INFORMATION:
54 (A) NAME: Dreger, Ginger
55 (B) REGISTRATION NUMBER: 33,055
56 (C) REFERENCE/DOCKET NUMBER: GENENT.33CP2C2
C--> 58 (ix) TELECOMMUNICATION INFORMATION:
59 (A) TELEPHONE: 949/760-0404
60 (B) TELEFAX: 949/760-9502
61 (2) INFORMATION FOR SEQ ID NO: 1:
63 (i) SEQUENCE CHARACTERISTICS:
64 (A) LENGTH: 3194 base pairs
65 (B) TYPE: Nucleic Acid
66 (C) STRANDEDNESS: Single
67 (D) TOPOLOGY: Linear
W--> 68 (ii) MOLECULE TYPE: nucleic acid

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Input Set : A:\Pto.amc

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70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

73 GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50
75 GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
77 CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
79 CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
81 TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
83 CGACCCCTTCT CCTGGCATCG TGGCATTTC GAGATTGGAG CCTAACAGTG 300
85 TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
87 GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400
89 GAAATTTGTG GATTCTGGAT TAAAATTTGT GGCTCATAAA GCATTTCTGA 450
91 AAAACAGCAA CCTGCAGCAC ATCAATTTTA CCCGAAACAA ACTGACGAGT 500
93 TTGTCTAGGA AACATTTCCG TCACCTTGAC TTGTCTGAAC TGATCCTGGT 550
95 GGGCAATCCA TTTACATGCT CCTGTGACAT TATGTGGATC AAGACTCTCC 600
97 AAGAGGCTAA ATCCAGTCCA GACACTCAGG ATTTGTACTG CCTGAATGAA 650
99 AGCAGCAAGA ATATTTCCCCT GGCAAACCTG CAGATACCCA ATTGTGGTTT 700
101 GCCATCTGCA AATCTGGCCG CACCTAACCT CACTGTGGAG GAAGGAAAGT 750
103 CTATCACATT ATCCTGTAGT GTGGCAGGTG ATCCGGTTCC TAATATGTAT 800
105 TGGGATGTTG GTAACCTGGT TTCCAAACAT ATGAATGAAA CAAGCCACAC 850
107 ACAGGGCTCC TTAAGGATAA CTAACATTTT ATCCGATGAC AGTGGGAAGC 900
109 AGATCTCTTG TGTGGCGGAA AATCTGTAG GAGAAGATCA AGATTCTGTC 950
111 AACCTCACTG TGCATTTTGC ACCAACTATC ACATTTCTCG AATCTCCAAC 1000
113 CTCAGACCAC CACTGGTGCA TTCCATTAC TGTGAAAGGC AACCACAAAC 1050
115 CAGCGCTTCA GTGGTTCTAT AACGGGGCAA TATTGAATGA GTCCAAATAC 1100
117 ATCTGTACTA AAATACATGT TACCAATCAC ACGGAGTACC ACGGCTGCCT 1150
119 CCAGCTGGAT AATCCCCTC ACATGAACAA TGGGGACTAC ACTCTAATAG 1200
121 CCAAGAATGA GTATGGGAAG GATGAGAAAC AGATTTCTGC TCACTTCATG 1250
123 GGCTGGCCTG GAATTGACGA TGGTGCAAAC CCAAATTATC CTGATGTAAT 1300
125 TTATGAAGAT TATGGAAGT CAGCGAATGA CATCGGGGAC ACCACGAACA 1350
127 GAAGTAATGA AATCCCCTCC ACAGACGTCA CTGATAAAAC CGGTCGGGAA 1400
129 CATCTCTCGG TCTATGCTGT GGTGGTGATT GCGTCTGTGG TGGGATTTTG 1450
131 CCTTTTGGTA ATGCTGTTTC TGCTTAAAGT GGCAAGACAC TCCAAGTTTG 1500
133 GCATGAAAGG CCCAGCCTCC GTTATCAGCA ATGATGATGA CTCTGCCAGC 1550
135 CCACTCCATC ACATCTCCAA TGGGAGTAAC ACTCCATCTT CTTCGGAAGG 1600
137 TGGCCAGAT GCTGTCATTA TTGGAATGAC CAAGATCCCT GTCATTGAAA 1650
139 ATCCCAGTA CTTTGGCATC ACCAACAGTC AGCTCAAGCC AGACACATTT 1700
141 GTTCAGCACA TCAAGCGACA TAACATTGTT CTGAAAAGGG AGCTAGGCCA 1750
143 AGGAGCCTTT GGAAAAGTGT TCCTAGCTGA ATGCTATAAC CTCTGTCCTG 1800
145 AGCAGGACAA GATCTTGGTG GCAGTGAAGA CCCTGAAGGA TGCCAGTGAC 1850
147 AATGCACGCA AGGACTTCCA CCGTGAGGCC GAGCTCCTGA CCAACCTCCA 1900
149 GCATGAGCAC ATCGTCAAGT TCTATGGCGT CTGCGTGGAG GGCGACCCCC 1950
151 TCATCATGGT CTTTGAGTAC ATGAAGCATG GGGACCTCAA CAAGTTCCTC 2000
153 AGGGCACACG GCCCTGATGC CGTGCTGATG GCTGAGGGCA ACCCGCCAC 2050
155 GGAAGTACG CAGTCGCAGA TGCTGCATAT AGCCAGCAG ATCGCCGCGG 2100
157 GCATGGTCTA CCTGGCGTCC CAGCACTTCG TGCACCGCGA TTTGGCCACC 2150
159 AGGAACTGCC TGGTCGGGGA GAACTTGCTG GTGAAAATCG GGGACTTTGG 2200
161 GATGTCCCGG GACGTGTACA GCACTGACTA CTACAGGGTC GGTGGCCACA 2250
163 CAATGCTGCC CATTCGCTGG ATGCCTCCAG AGAGCATCAT GTACAGGAAA 2300
165 TTCACGACGG AAAGCGACGT CTGGAGCCTG GGGGTCGTGT TGTGGGAGAT 2350
167 TTTCACCTAT GGCAAACAGC CCTGGTACCA GCTGTCAAAC AATGAGGTGA 2400

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Input Set : A:\Pto.amc

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169 TAGAGTGTAT CACTCAGGGC CGAGTCCTGC AGCGACCCCG CACGTGCCCC 2450
171 CAGGAGGTGT ATGAGCTGAT GCTGGGGTGC TGGCAGCGAG AGCCCCACAT 2500
173 GAGGAAGAAC ATCAAGGGCA TCCATACCCCT CCTTCAGAAC TTGGCCAAGG 2550
175 CATCTCCGGT CTACCTGGAC ATTCTAGGCT AGGGCCCTTT TCCCCAGACC 2600
177 GATCCTTCCC AACGTACTCC TCAGACGGGC TGAGAGGATG AACATCTTTT 2650
179 AACTGCCGCT GGAGGCCACC AAGCTGCTCT CCTTCACTCT GACAGTATTA 2700
181 ACATCAAAGA CTCCGAGAAG CTCTCGAGGG AAGCAGTGTG TACTTCTTCA 2750
183 TCCATAGACA CAGTATTGAC TTCTTTTGG CATTATCTCT TTCTCTCTTT 2800
185 CCATCTCCCT TGGTTGTTCC TTTTCTTTT TTTAAATTTT CTTTTCTTTC 2850
187 TTTTTTTTCG TCTTCCCTGC TTCACGATTC TTACCTTTC TTTTGAATCA 2900
189 ATCTGGCTTC TGCATTACTA TTAACCTGTC ATAGACAAAG GCCTTAACAA 2950
191 ACGTAATTTG TTATATCAGC AGACACTCCA GTTTGCCAC CACAATAAC 3000
193 AATGCCTTGT TGTATTCTCG CCTTTGATGT GGATGAAAAA AAGGGAAAAAC 3050
195 AAATATTTCA CTAAACTTT GTCACCTCTG CTGTACAGAT ATCGAGAGTT 3100
197 TCTATGGATT CACTTCTATT TATTTATTAT TATTACTGTT CTTATTGTTT 3150
199 TTGGATGGCT TAAGCCTGTG TATAAAAAAA AAAAAAATC TAGA 3194

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201 (2) INFORMATION FOR SEQ ID NO: 2:

203 (i) SEQUENCE CHARACTERISTICS:

204 (A) LENGTH: 822 amino acids

205 (B) TYPE: Amino Acid

206 (D) TOPOLOGY: Linear

208 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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210 Met Ser Ser Trp Ile Arg Trp His Gly Pro Ala Met Ala Arg Leu
211 1 5 10 15
213 Trp Gly Phe Cys Trp Leu Val Val Gly Phe Trp Arg Ala Ala Phe
214 20 25 30
216 Ala Cys Pro Thr Ser Cys Lys Cys Ser Ala Ser Arg Ile Trp Cys
217 35 40 45
219 Ser Asp Pro Ser Pro Gly Ile Val Ala Phe Pro Arg Leu Glu Pro
220 50 55 60
222 Asn Ser Val Asp Pro Glu Asn Ile Thr Glu Ile Phe Ile Ala Asn
223 65 70 75
225 Gln Lys Arg Leu Glu Ile Ile Asn Glu Asp Asp Val Glu Ala Tyr
226 80 85 90
228 Val Gly Leu Arg Asn Leu Thr Ile Val Asp Ser Gly Leu Lys Phe
229 95 100 105
231 Val Ala His Lys Ala Phe Leu Lys Asn Ser Asn Leu Gln His Ile
232 110 115 120
234 Asn Phe Thr Arg Asn Lys Leu Thr Ser Leu Ser Arg Lys His Phe
235 125 130 135
237 Arg His Leu Asp Leu Ser Glu Leu Ile Leu Val Gly Asn Pro Phe
238 140 145 150
240 Thr Cys Ser Cys Asp Ile Met Trp Ile Lys Thr Leu Gln Glu Ala
241 155 160 165
243 Lys Ser Ser Pro Asp Thr Gln Asp Leu Tyr Cys Leu Asn Glu Ser
244 170 175 180
246 Ser Lys Asn Ile Pro Leu Ala Asn Leu Gln Ile Pro Asn Cys Gly
247 185 190 195
249 Leu Pro Ser Ala Asn Leu Ala Ala Pro Asn Leu Thr Val Glu Glu

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Input Set : A:\Pto.amc

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250		200		205		210
252	Gly Lys Ser Ile Thr Leu Ser Cys Ser Val Ala Gly Asp Pro Val					
253		215		220		225
255	Pro Asn Met Tyr Trp Asp Val Gly Asn Leu Val Ser Lys His Met					
256		230		235		240
258	Asn Glu Thr Ser His Thr Gln Gly Ser Leu Arg Ile Thr Asn Ile					
259		245		250		255
261	Ser Ser Asp Asp Ser Gly Lys Gln Ile Ser Cys Val Ala Glu Asn					
262		260		265		270
264	Leu Val Gly Glu Asp Gln Asp Ser Val Asn Leu Thr Val His Phe					
265		275		280		285
267	Ala Pro Thr Ile Thr Phe Leu Glu Ser Pro Thr Ser Asp His His					
268		290		295		300
270	Trp Cys Ile Pro Phe Thr Val Lys Gly Asn Pro Lys Pro Ala Leu					
271		305		310		315
273	Gln Trp Phe Tyr Asn Gly Ala Ile Leu Asn Glu Ser Lys Tyr Ile					
274		320		325		330
276	Cys Thr Lys Ile His Val Thr Asn His Thr Glu Tyr His Gly Cys					
277		335		340		345
279	Leu Gln Leu Asp Asn Pro Thr His Met Asn Asn Gly Asp Tyr Thr					
280		350		355		360
282	Leu Ile Ala Lys Asn Glu Tyr Gly Lys Asp Glu Lys Gln Ile Ser					
283		365		370		375
285	Ala His Phe Met Gly Trp Pro Gly Ile Asp Asp Gly Ala Asn Pro					
286		380		385		390
288	Asn Tyr Pro Asp Val Ile Tyr Glu Asp Tyr Gly Thr Ala Ala Asn					
289		395		400		405
291	Asp Ile Gly Asp Thr Thr Asn Arg Ser Asn Glu Ile Pro Ser Thr					
292		410		415		420
294	Asp Val Thr Asp Lys Thr Gly Arg Glu His Leu Ser Val Tyr Ala					
295		425		430		435
297	Val Val Val Ile Ala Ser Val Val Gly Phe Cys Leu Leu Val Met					
298		440		445		450
300	Leu Phe Leu Leu Lys Leu Ala Arg His Ser Lys Phe Gly Met Lys					
301		455		460		465
303	Gly Pro Ala Ser Val Ile Ser Asn Asp Asp Asp Ser Ala Ser Pro					
304		470		475		480
306	Leu His His Ile Ser Asn Gly Ser Asn Thr Pro Ser Ser Ser Glu					
307		485		490		495
309	Gly Gly Pro Asp Ala Val Ile Ile Gly Met Thr Lys Ile Pro Val					
310		500		505		510
312	Ile Glu Asn Pro Gln Tyr Phe Gly Ile Thr Asn Ser Gln Leu Lys					
313		515		520		525
315	Pro Asp Thr Phe Val Gln His Ile Lys Arg His Asn Ile Val Leu					
316		530		535		540
318	Lys Arg Glu Leu Gly Glu Gly Ala Phe Gly Lys Val Phe Leu Ala					
319		545		550		555
321	Glu Cys Tyr Asn Leu Cys Pro Glu Gln Asp Lys Ile Leu Val Ala					
322		560		565		570

RAW SEQUENCE LISTING

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Input Set : A:\Pto.amc

Output Set: N:\CRF3\08282001\I724524.raw

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324 Val Lys Thr Leu Lys Asp Ala Ser Asp Asn Ala Arg Lys Asp Phe
325                               575                               580                               585
327 His Arg Glu Ala Glu Leu Leu Thr Asn Leu Gln His Glu His Ile
328                               590                               595                               600
330 Val Lys Phe Tyr Gly Val Cys Val Glu Gly Asp Pro Leu Ile Met
331                               605                               610                               615
333 Val Phe Glu Tyr Met Lys His Gly Asp Leu Asn Lys Phe Leu Arg
334                               620                               625                               630
336 Ala His Gly Pro Asp Ala Val Leu Met Ala Glu Gly Asn Pro Pro
337                               635                               640                               645
339 Thr Glu Leu Thr Gln Ser Gln Met Leu His Ile Ala Gln Gln Ile
340                               650                               655                               660
342 Ala Ala Gly Met Val Tyr Leu Ala Ser Gln His Phe Val His Arg
343                               665                               670                               675
345 Asp Leu Ala Thr Arg Asn Cys Leu Val Gly Glu Asn Leu Leu Val
346                               680                               685                               690
348 Lys Ile Gly Asp Phe Gly Met Ser Arg Asp Val Tyr Ser Thr Asp
349                               695                               700                               705
351 Tyr Tyr Arg Val Gly Gly His Thr Met Leu Pro Ile Arg Trp Met
352                               710                               715                               720
354 Pro Pro Glu Ser Ile Met Tyr Arg Lys Phe Thr Thr Glu Ser Asp
355                               725                               730                               735
357 Val Trp Ser Leu Gly Val Val Leu Trp Glu Ile Phe Thr Tyr Gly
358                               740                               745                               750
360 Lys Gln Pro Trp Tyr Gln Leu Ser Asn Asn Glu Val Ile Glu Cys
361                               755                               760                               765
363 Ile Thr Gln Gly Arg Val Leu Gln Arg Pro Arg Thr Cys Pro Gln
364                               770                               775                               780
366 Glu Val Tyr Glu Leu Met Leu Gly Cys Trp Gln Arg Glu Pro His
367                               785                               790                               795
369 Met Arg Lys Asn Ile Lys Gly Ile His Thr Leu Leu Gln Asn Leu
370                               800                               805                               810
372 Ala Lys Ala Ser Pro Val Tyr Leu Asp Ile Leu Gly
373                               815                               820                               822

```

375 (2) INFORMATION FOR SEQ ID NO: 3:

377 (i) SEQUENCE CHARACTERISTICS:

378 (A) LENGTH: 1870 base pairs

379 (B) TYPE: Nucleic Acid

380 (C) STRANDEDNESS: Single

381 (D) TOPOLOGY: Linear

383 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```

386 GGAAGGTTTA AAGAAGAAGC CGCAAAGCGC AGGGAAGGCC TCCCGGCACG 50
388 GGTGGGGGAA AGCGGCCGGT GCAGCGCGGG GACAGGCACT CGGGCTGGCA 100
390 CTGGCTGCTA GGGATGTCGT CCTGGATAAG GTGGCATGGA CCCGCCATGG 150
392 CGCGGCTCTG GGGCTTCTGC TGGCTGGTTG TGGGCTTCTG GAGGGCCGCT 200
394 TTCGCCTGTC CCACGTCCTG CAAATGCAGT GCCTCTCGGA TCTGGTGCAG 250
396 CGACCCTTCT CCTGGCATCG TGGCATTTCC GAGATTGGAG CCTAACAGTG 300
398 TAGATCCTGA GAACATCACC GAAATTTTCA TCGCAAACCA GAAAAGGTTA 350
400 GAAATCATCA ACGAAGATGA TGTGAAGCT TATGTGGGAC TGAGAAATCT 400

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VERIFICATION SUMMARY

DATE: 08/28/2001

PATENT APPLICATION: US/09/724,524

TIME: 18:05:32

Input Set : A:\Pto.amc

Output Set: N:\CRF3\08282001\I724524.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:30 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:45 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:49 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:53 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:58 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]
L:68 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=1